RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:	09/545,998B
Source:	1FW16
Date Processed by STIC:	8/10/05
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GREE ERRORS ECLICATION WAS STATED AS

Number: _0	09/545,998 <i>6</i>		CRF Edit Date: 8//6 Edited by:
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	ucleic acid/amino ac ed" to the next line	id numbers/text	t in cases where the sequ
		, ,	
Corrected th	he SEQ ID NO. Sequ	uence numbers	edited were:
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Other:			•

Revised 09/09/2003



IFW16

RAW SEQUENCE LISTING DATE: 08/10/2005
PATENT APPLICATION: US/09/545,998B TIME: 14:51:48

Input Set : N:\AMC\PTO.AMC.txt

Output Set: N:\CRF4\08102005\I545998B.raw

SEQUENCE LISTING

```
(1) GENERAL INFORMATION:
      6
             (i) APPLICANT: Gorman, Daniel M.
      7
                             Randall, Troy D.
      8
                             Zlotnik, Albert
     10
            (ii) TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
                                      REAGENTS
     11
           (iii) NUMBER OF SEQUENCES: 9
     13
     15
            (iv) CORRESPONDENCE ADDRESS:
                   (A) ADDRESSEE: DNAX Research Institute
     16
                  (B) STREET: 901 California Avenue
     17
                  (C) CITY: Palo Alto
     18
     19
                  (D) STATE: California
                  (E) COUNTRY: USA
     20
                  (F) ZIP: 94304-1104
     21
     23
             (v) COMPUTER READABLE FORM:
     24
                   (A) MEDIUM TYPE: CD-R
     25
                   (B) COMPUTER: IBM PC compatible
     26
                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     27
                   (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
     29
            (vi) CURRENT APPLICATION DATA:
C--> 30
                   (A) APPLICATION NUMBER: US/09/545,998B
C--> 31
                   (B) FILING DATE: 10-Apr-2000
     32
                  (C) CLASSIFICATION:
           (vii) PRIOR APPLICATION DATA:
     42
     35
                   (A) APPLICATION NUMBER: US 08/911,423
     36
                  (B) FILING DATE: 16-AUG-1996
     39
                  (A) APPLICATION NUMBER: US 60/023,419
                  (B) FILING DATE: 16-AUG-1996
     40
     43
                  (A) APPLICATION NUMBER: US 60/027,901
     44
                  (B) FILING DATE: 07-OCT-1996
     46
          (viii) ATTORNEY/AGENT INFORMATION:
     47
                   (A) NAME: Hill, Laurie L.
     48
                  (B) REGISTRATION NUMBER: 51,804
     49
                  (C) REFERENCE/DOCKET NUMBER: 140942000510
     51
            (ix) TELECOMMUNICATION INFORMATION:
     52
                  (A) TELEPHONE: 858-720-5100
     53
                  (B) TELEFAX: 858-720-5125
       (2) INFORMATION FOR SEQ ID NO: 1:
     58
             (i) SEQUENCE CHARACTERISTICS:
     59
                  (A) LENGTH: 1073 base pairs
     60
                  (B) TYPE: nucleic acid
     61
                  (C) STRANDEDNESS: single
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RAW SEQUENCE LISTING DATE: 08/10/2005 PATENT APPLICATION: US/09/545,998B TIME: 14:51:48

Input Set : N:\AMC\PTO.AMC.txt

62			(D) TC	POLC	GY:	line	ar									
64		(ii)	MOL	ECUL	E TY	PE:	CDNA										
67	•	(ix)	FEA	TURE	:												
68			(A) NA	ME/K	EY:	CDS										
69							68	751									
72		(xi)	SEC						EO I	D NO): 1:						
	CTCG		~						~				ACAG	AA C	ACTO	CAGGAG	60
			ATG														109
77							Ala										
78			1	1			5			-1-	1	10				-1-	
	GTG	CTG	GAC	CTA	GGT	CAG	CCG	AGT	GTA	GTT	GAG	GAG	CCT	GGC	TGT	GGC	157
			Asp														
82	15		,		2	20					25				1	30	
		GGC	AAG	GTT	CAG		GGA	AGT	GGC	AAC		ACT	CGC	TGC	TGC		205
			Lys														
86		-	-		35		-		1	40			,	-	45		
	CTG	TAT	GCT	CCA	GGC	AAG	GAG	GAC	TGT	CCA	AAA	GAA	AGG	TGC	ATA	TGT	253
			Ala														
90		-		50	•	•		•	55		•		_	60		-	
92	GTC	ACA	CCT	GAG	TAC	CAC	TGT	GGA		CCT	CAG	TGC	AAG		TGC	AAG	301
			Pro														
94			65		4		- 2	70	- 1				75		- 4	4	
96	CAC	TAC	CCC	TGC	CAA	CCA	GGC	CAG	AGG	GTG	GAG	TCT	CAA	GGG	GAT	ATT	349
			Pro														
98		80		•			85		-			90		•	-		
100	GTG	TTT	GGC	TTC	. CGG	TGT	GTT	GCC	TGT	GCC	ATG	GGC	ACC	TTC	TCC	GCA	397
																Ala	
102			-		_	100			•		105	_				110	
104	GGT	' CGT	GAC	GGI	CAC	TGC	AGA	CTT	' TGG	ACC	: AAC	TGT	TCI	' CAC	TT	GGA	445
105	Gly	Arc	Asp	Gly	His	Cys	Arg	Leu	Trp	Thr	Asn	Cys	Ser	Glr	ı Phe	e Gly	
106	_		_	_	115	_	_		_	120		-			125	_	
108	TTT	CTC	ACC	ATG	TTC	CCI	GGG	AAC	. AAG	ACC	CAC	AAT	GCI	GTC	TGO	ATC	493
109	Phe	Lei	Thr	Met	Phe	Pro	Gly	Asn	Lys	Thr	His	Asn	Ala	. Val	Cys	: Ile	
110)			130)		_		135	<u>;</u>				140)		
112	CCG	GAC	CCA	CTG	CCC	ACI	GAG	CAA	TAC	GGC	CAT	TTG	ACT	GTC	ATO	TTC	541
113	Pro	Gli	ı Pro	Leu	Pro	Thr	Glu	Gln	Tyr	Gly	His	Leu	Thr	· Val	Ile	e Phe	
114	1		145					150	ı				155				
116	CTG	GTO	ATG	GCT	GCA	TGC	: ATT	TTC	TTC	CTA	ACC	ACA	GTC	CAC	CTC	GGC	589
117	Leu	Va]	. Met	Ala	Ala	Cys	Ile	Phe	Phe	Leu	Thr	Thr	Val	Glr	ı Leı	ıGly	
118	}	160)				165					170					
120	CTG	CAC	: ATA	TGG	CAG	CTG	AGG	AGG	CAA	CAC	ATG	TGT	CCC	CGF	A GAC	ACC	637
																ı Thr	
	175			_		180	_	_			185	_				190	
124	CAG	CC	TTC	GCG	GAG	GTG	CAG	TTG	TCA	GCI	' GAG	GAT	GCI	TGC	AGO	TTC	685
																Phe	
126			•		195					200		-		-	205		
128	CAG	TTC	CCT	GAG	GAG	GAA	CGC	GGG	GAG	CAG	ACA	GAA	GAA	AAC	TGT	CAT	733
																His	
130				210			_	-	215					220	-		

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PATENT APPLICATION: US/09/545,998B TIME: 14:51:48

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				CGG			TGA	GGCC'	rgg :	rctt(CCTC'	rg To	GCCC	CAAG	С		781
	33 Leu Gly Gly Arg Trp Pro																
134																	
	6 CAGACGCTAC AAGACTTGCC CAGCTATACC CTTGGTGAGA GCAGGGGCCA TGCTCTGCAC											841					
	8 CCTTCCCTGG GCCTGGCCCT GCTCCCCTCA ACAGTGGCGG AAGTGGGTGT ATGAGAGCGG												901				
	O TGAGTTACGA TTGGGCCCTA TGGCTGCCTT TCTCATTTGA CAGCTCTGTT GGAGTAGGGT												961				
	42 CTTTGGGCCC ACCAAGAGCA CCACGTTTAG CACAAGATCT TGTACAAGAA TAAATACTTG												1021				
	144 TTTAGTAACC TGAAAAAAAA AAAAAAAAGG GCGGCCGCGG AGGCCGAATT CC 1													1073			
	(2)					-											
	149 (i) SEQUENCE CHARACTERISTICS:																
	150 (A) LENGTH: 228 amino acids																
	(B) TYPE: amino acid																
154	152 (D) TOPOLOGY: linear 154 (ii) MOLECULE TYPE: protein																
154				QUEN			_		משם	אור אור	.						
				Trp									T AU	Cvc	17-1	Len	
159	1	Gry	AIG	тър	5	Met	пец	ıyı	Gry	10	Ser	Mec	neu	Cys	15	шeu	
		Len	Glv	Gln		Ser	Val	Val	Glu		Pro	Glv	Cvs	Glv		Glv	
162	1101	шец	OI,	20	110	501	V 4 1	Vu_	25	Olu	110	O ₁	Cyb	30	110	Oly	
	Lvs	Val	Gln	Asn	Glv	Ser	Glv	Asn		Thr	Ara	Cvs	Cvs		Len	Tyr	
165			35			001	017	40	71011		**** 9	Cyb	45	501	200	- / -	
	Ala	Pro		Lys	Glu	Asp	Cvs		Lvs	Glu	Ara	Cvs		Cvs	Val	Thr	
168		50		-1-			55		-10			60		0,2			
	Pro			His	Cvs	Glv		Pro	Gln	Cvs	Lvs		Cvs	Lvs	His	Tvr	
171			-1-		-1-	70	F			-1-	75		-1-	-1-		80	
		Cys	Gln	Pro	Gly		Arq	Val	Glu	Ser		Glv	Asp	Ile	Val		
174		•		•	85		,			90		*	•		95		
176	Gly	Phe	Arg	Cys	Val	Ala	Cys	Ala	Met	Gly	Thr	Phe	Ser	Ala	Gly	Arq	
177	-		_	100			_		105	_				110	_	_	
179	Asp	Gly	His	Cys	Arg	Leu	Trp	Thr	Asn	Cys	Ser	Gln	Phe	Gly	Phe	Leu	
180			115					120					125				
182	Thr	Met	Phe	Pro	Gly	Asn	Lys	Thr	His	Asn	Ala	Val	Cys	Ile	Pro	Glu	
183		130					135					140					
185	Pro	Leu	Pro	Thr	Glu	Gln	Tyr	Gly	His	Leu	Thr	Val	Ile	Phe	Leu	Val	
	145					150					155					160	
188	Met	Ala	Ala	Cys	Ile	Phe	Phe	Leu	Thr	Thr	Val	Gln	Leu	Gly	Leu	His	
189					165					170					175		
	Ile	Trp	Gln	Leu	Arg	Arg	Gln	His	Met	Cys	Pro	Arg	Glu	Thr	Gln	Pro	
192	_	_		180	_				185					190			
	Phe	Ala		Val	Gln	Leu	Ser		Glu	Asp	Ala	Cys		Phe	Gln	Phe	
195	_		195	_		_	_	200		_			205			_	
	Pro		Glu	Glu	Arg	Gly		Gln	Thr	Glu	Glu		Cys	His	Leu	Gly	
198		210	_	_			215					220					
		Arg	Trp	Pro													
	225	T		DT 63 -				••	_								
	(2)			rion													
205		(1		QUENC													
206				A) LI					_	S							
207			(1	B) T	(PE:	nuc.	reic	acı	1								

RAW SEQUENCE LISTING DATE: 08/10/2005
PATENT APPLICATION: US/09/545,998B TIME: 14:51:48

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211					LE TY	(PE:	CDIVA	4									
214																	
215																	
216																	
219																	
	ATG																48
222	Met	Ala	Gln	His	Gly	Ala	Met	Gly	Ala	Phe	Arg	Ala	Leu	Cys	Gly	Leu	
223	1				5					10					15		
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226	Ala	Leu	Leu	Cys	Ala	Leu	Ser	Leu	Gly	Gln	Arg	Pro	Thr	Gly	Gly	Pro	
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229	GGG	TGC	GGC	CCT	GGG	CGC	CTC	CTG	CTT	GGG	ACG	GGA	ACG	GAC	GCG	CGC	144
230	Gly	Cys	Gly	Pro	Gly	Arg	Leu	Leu	Leu	Gly	Thr	Gly	Thr	Asp	Ala	Arg	
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235	Cys	Cys	Arg	Val	His	Thr	Thr	Arg	Cys	Cys	Arg	Asp	Tyr	Pro	Gly	Glu	
236		50					55					60					
	GAG																240
239	Glu	Cys	Cys	Ser	Glu	${\tt Trp}$	Asp	Cys	Met	Cys	Val	Gln	Pro	Glu	Phe	His	
240	65					70					75					80	
	TGC																288
243	Cys	Gly	Asp	Pro	Cys	Cys	Thr	Thr	Cys	Arg	His	His	Pro	Cys	Pro	Pro	
244					85					90					95		
	GGC																336
	Gly	Gln	Gly		Gln	Ser	Gln	Gly	_	Phe	Ser	Phe	Gly		Gln	Cys	
248				100					105					110			
	ATC																384
	Ile	Asp	_	Ala	Ser	Gly	Thr		Ser	Gly	Gly	His		Gly	His	Cys	
252			115					120					125				
	AAA -																432
	Lys		Trp	Thr	Asp	Cys		GIn	Phe	GIA	Phe		Thr	Val	Phe	Pro	
256		130					135					140			~~~		
	GGG																480
	Gly	Asn	гÀг	Inr	His		Ата	vai	Cys	Val		GIY	ser	Pro	Pro		
	145					150					155					160	
	GAG																528
	Glu	Pro	Leu	GIY	_	Leu	Thr	Val	Val		Leu	Ala	Val	Ala		Cys	
264	~~~	~~~	~~~	~~~	165			~- ~		170	~-~	~- ~			175	~~~	
	GTC																576
	Val	Leu	Leu		Thr	Ser	Ala	GIn		GIY	Leu	His	Ile	_	GIn	Leu	
268				180					185					190			
	AGG																624
	Arg	ser		Cys	Met	Trp	Pro	_	Glu	Thr	GIn	ьeu		ьeu	Glu	val	
272	000	~~~	195		a- -		~~-	200			a		205	~-~		~-	
	CCG																672
	Pro		Ser	Thr	Glu	Asp		Arg	Ser	Cys	GIn		Pro	Glu	Glu	GIu	
276		210					215					220					

RAW SEQUENCE LISTING DATE: 08/10/2005
PATENT APPLICATION: US/09/545,998B TIME: 14:51:48

Input Set : N:\AMC\PTO.AMC.txt

280 225 230 240 282 267 TGAGCCTGCC CGTCCTCCGG GGCCACCCAGC CCCTCCCCAGC 282 283 CGT TGAGCCTGCC CGTCCTCCGG GGCCACCCAGC CCCTCCCCAGC 283 AGCACCACCAG GGCCGCAGGG GCTCTGCGTT CTGCTCTGGG CCGGCCCTGCCCCGG 284 GAGCTCCCCA GGCCGCAGGA GGTGCAGTG ACCACCGCC TGGACCATGC ACTTCCGCGG 285 GAGCCACCATAA TCAATTCAC TGCCGTGGT TTTACCAACGT CCTCATAGCT CTTCTATAGT 296 CCGCTCTAAA GGATCCAAGC TTACCTACGC GTGCATGCGA CCTCATAGCT CTTCTATAGT 297 (i) SEQUENCE CHARACTERISTICS: 298 (A) LENGTH: 241 amino acids 299 (B) TYPE: amino acids 299 (B) TYPE: amino acids 300 (D) TOPOLOGY: linear 301 (ii) MOLECULE TYPE: protein 304 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4: 305 Met Ala Gin His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu 307 1 5 10 15 308 Ala Leu Leu Cys Ala Leu Ser Leu Gly Gin Arg Pro Thr Gly Gly Pro 310 20 25 30 312 Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg 313 35 40 36 315 Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu 316 50 55 60 318 Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His 319 65 70 75 80 321 Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro 322 85 90 95 324 Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys 325 100 105 110 326 Glu Pro Leu Gly Trp Leu Thr Val Phe Pro 327 11 Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys 328 115 120 125 140 333 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala 331 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala 332 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala 333 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala 340 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys 337 165 170 348 Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val 340 195 220 345 Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu 346 Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val 341 195 220 342 Gly Glu Arg Ser Ala Glu Leu Sel Gly Arg Leu Gly Asp Leu Trp 348 Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp 349 225	279	Arg			CGA Arg		Ala					Arg					Trp	720
286 GAGCTCCCCA GGCCGCAGGG GTTCTGCGTT CTGCTCTGGC CCGGGCCTG CTCCCCTGGC 288 AGCAGAAGTG GGTGCCAGGA GGTGGCAGTG ACCAGGCCCC TGGACCATGC AGTTCGGGG 280 CCGCTCTAAA GGATCCAAGC TTACGTACGC GTGCATGGA CCTCATAGCT CTTCTATAGT 290 CCGCTCTAAA GATCCAGCC TTACGTACGC GTGCATGGA CCTCATAGCT CTTCTATAGT 291 GTACCCTAAA TTCAATTCAC TGGCCGTGGT TTTACAAGT CCTGACTGGG AAA 292 (i) SEQUENCE CHARACTERISTICS: 298 (A) LENGTH: 241 amino acids 300 (D) TOPOLOGY: linear 302 (ii) MOLECULE TYPE: protein 304 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4: 306 Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu 307 1 5 10 15 15 309 Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro 310 20 25 30 312 Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg 313 35 40 45 315 Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu 316 50 55 60 318 Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Gly Phe His 319 65 70 70 75 60 321 Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro 322 80 90 95 324 Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys 325 100 105 100 327 Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys 328 115 120 125 330 Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Gly Phe Glr Cys 331 130 135 140 333 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala 334 145 150 155 339 Val Leu Leu Chy Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys 337 165 170 339 Val Leu Leu Chy Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys 337 165 170 342 Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Glu Val 343 195 200 205 345 Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu 346 210 215 220 348 Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp 349 225 230 235 240 351 Val 351 Val 351 Val 351 Val 351 Val 352 110 107 107 107 107 107 107 107 107 107			TGA	GCCT(GGC (CGTC	230 CTCC	GG GG	GCCA	CCGA	C CGC	235 CAGC(CAGC	CCC	rccc	CAG	240	773
288 AGCAGAAGG GGTCCAGGAA GGTGCAGTG ACCAGCGCC TGGACCATGC AGTTCGCGG 995 290 CCGCTCTAAA GGATCCAAGC TTACGTAGCG GTGCAGTGCA	283																	
290 CCGCTCTAAA GGATCCAAGC TTACGTACGC GTGCATGCGA CGTCATAGCT CTTCTATAGT 292 GTCACCTAAA TTCAATTCAC TGGCCGTCGT TTTACAACGT CCTGACTGGG AAA 1006 295 (2) INFORMATION FOR SEQ ID NO: 4: 297	286													833				
990 CCGCTCTAAA GGATCCAAGC TTACGTACGC GTGCATGCGA CGTCATAGCT CTTCTATAGT 292 GTCACCTAAA TTCAATTCAC TGGCCGTCGT TTTACAACGT CCTGACTGGG AAA 1006 295 (2) INFORMATION FOR SEQ ID NO: 4: 297	288	8 AGCAGAAGTG GGTGCAGGAA GGTGGCAGTG ACCAGCGCCC TGGACCATGC AGTTCGGCGG													893			
295 (2) INFORMATION FOR SEQ ID NO: 4: 297																		
295 (2) INFORMATION FOR SEQ ID NO: 4: 297 (i) SEQUENCE CHARACTERISTICS: 298 (A) LENGTH: 241 amino acids 299 (B) TYPE: amino acids 300 (D) TOPOLOGY: linear 301 (ii) MOLECULE TYPE: protein 302 (iii) MOLECULE TYPE: protein 303 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4: 306 Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu 307 1 1 50 15 309 Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro 310 20 25 30 312 Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg 313 35 40 45 315 Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu 316 50 55 60 318 Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His 319 65 70 75 80 321 Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro 322 85 90 95 324 Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys 325 100 105 105 326 116 Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys 327 11e Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys 328 115 130 135 140 333 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro 331 130 135 140 333 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala 334 145 150 335 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys 337 165 170 175 348 Arg Gly Glu Arg Ser Ala Glu Glu Leu Gly Leu His Ile Trp Gln Leu 340 180 180 180 185 100 190 342 Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Glu Glu 346 Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu Glu 346 Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu 346 Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu 347 Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu 348 Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp 349 225 230 230 235 240																		
298 (A) LENGTH: 241 amino acids 299 (B) TYPE: amino acids 300 (D) TOPOLOGY: linear 302 (ii) MOLECULE TYPE: protein 304 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4: 306 Met Ala GIn His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu 307 1 5 10 15 309 Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro 310 20 25 30 312 Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg 313 35 40 45 315 Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu 316 50 55 80 318 Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His 319 65 70 75 80 321 Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro 322 90 95 324 Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys 325 100 327 Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys 326 115 120 125 330 Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro 331 130 135 136 155 160 334 145 150 150 140 335 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala 336 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Leu Ala Val Ala Ala Ala Cys 337 165 170 175 339 Val Leu Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu 340 180 185 195 200 345 Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu Glu 346 Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp 349 225 230 235 235 240	295																	
298 (A) LENGTH: 241 amino acids 299 (B) TYPE: amino acids 300 (D) TOPOLOGY: linear 302 (ii) MOLECULE TYPE: protein 304 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4: 306 Met Ala GIn His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu 307 1 5 10 15 309 Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro 310 20 25 30 312 Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg 313 35 40 45 315 Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu 316 50 55 80 318 Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His 319 65 70 75 80 321 Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro 322 90 95 324 Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys 325 100 327 Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys 326 115 120 125 330 Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro 331 130 135 136 155 160 334 145 150 150 140 335 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala 336 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Leu Ala Val Ala Ala Ala Cys 337 165 170 175 339 Val Leu Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu 340 180 185 195 200 345 Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu Glu 346 Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp 349 225 230 235 235 240	297	297 (i) SEQUENCE CHARACTERISTICS:																
10	298																	
302	299																	
304	300																	
304	302																	
Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu 15 10 15 15	_																	
307														Leu	Cys	Gly	Leu	
309 Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro 310 30 312 Gly Cys Gly Pro Gly Arg Leu Leu Gly Thr Gly Thr Asp Ala Arg Ala						_			2			J			- 4	_		
310			Leu	Leu	Cvs	Ala	Leu	Ser	Leu	Glv		Ara	Pro	Thr	Glv	Glv	Pro	
312 Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg 313					-					-		5			•	2		
313		Glv	Cvs	Glv		Glv	Ara	Leu	Leu		Glv	Thr	Glv	Thr	Asp	Ala	Ara	
315 Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu 316		1	-1-			2	5				1		1				- · · · · J	
316		Cvs	Cvs	Ara	Val	His	Thr	Thr		Cvs	Cvs	Ara	Asp	Tvr	Pro	Glv	Glu	
318 Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His 319 65		-1-	_	5					5	-1-	- 2	5		- 1		1		
319 65		Glu		Cvs	Ser	Glu	Trp		Cvs	Met	Cvs	Val		Pro	Glu	Phe	His	
321 Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro 322			-1	-1					-1-		-1-							
322			Glv	Asp	Pro	Cvs	Cvs	Thr	Thr	Cvs	Ara	His	His	Pro	Cvs	Pro		
324 Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys 325		-1	1				-1-			-1-	_				- 2 -			
325		Gly	Gln	Glv	Val	Gln	Ser	Gln	Glv	Lvs	Phe	Ser	Phe	Gly	Phe	Gln	Cys	
327 The Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys 328 115 120 120 125 125 125 125 1330 Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro 331 130 130 135 135 135 140 140 140 140 140 1333 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala Ala Cys 336 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys 337 165 165 170 175 175 175 175 139 Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu 340 185 185 190				4					-	_				-			•	•
328 115 120 125 330 Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro 331 130 135 140 333 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala 334 145 150 155 160 336 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Leu Leu Ala Val Ala Ala Cys 337 165 170 175 339 Val Leu Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu 340 180 185 190 342 Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Leu Glu Val 343 195 200 345 Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu Glu 346 210 215 348 Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp 349 225 230 351 Val 354 (2) 354 (2) 354 (2) 354 (2)	327	Ile	Asp	Cys	Ala	Ser	Gly	Thr	Phe	Ser	Gly	Gly	His	Glu	Gly	His	Cys	
331			-	-			•				•	•			•		-	
331	330	Lys	Pro	Trp	Thr	Asp	Cys	Thr	Gln	Phe	Gly	Phe	Leu	Thr	Val	Phe	Pro	
334 145		•		-		-	•				-							
334 145	333	Gly	Asn	Lys	Thr	His	Asn	Ala	Val	Cys	Val	Pro	Gly	Ser	Pro	Pro	Ala	
337		_		-						-			-					
337	336	Glu	Pro	Leu	Gly	Trp	Leu	Thr	Val	Val	Leu	Leu	Ala	Val	Ala	Ala	Cys	
340					-													
340	339	Val	Leu	Leu	Leu	Thr	Ser	Ala	Gln	Leu	Gly	Leu	His	Ile	Trp	Gln	Leu	
343																		
343	342	Arq	Ser	Gln	Cys	Met	Trp	Pro	Arg	Glu	Thr	Gln	Leu	Leu	Leu	Glu	Val	
345 Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu 346 210 225 220 2348 Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp 349 225 230 235 240 351 Val 354 (2) INFORMATION FOR SEQ ID NO: 5:					•		-											
346 210 215 220 348 Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp 349 225 230 235 240 351 Val 354 (2) INFORMATION FOR SEQ ID NO: 5:	345	Pro	Pro	Ser	Thr	Glu	Asp	Ala		Ser	Cys	Gln	Phe	Pro	Glu	Glu	Glu	
349 225 230 235 240 351 Val 354 (2) INFORMATION FOR SEQ ID NO: 5:							•				-							
349 225 230 235 240 351 Val 354 (2) INFORMATION FOR SEQ ID NO: 5:	348	Arq	Gly	Glu	Arq	Ser	Ala	Ġlu	Glu	Lys	Gly	Arq	Leu	Gly	Asp	Leu	Trp	
351 Val 354 (2) INFORMATION FOR SEQ ID NO: 5:		_	-							-	-			•	•			
354 (2) INFORMATION FOR SEQ ID NO: 5:																		
			INF	ORMA!	TION	FOR	SEQ	ID 1	90: 5	5:								
																	·	

VERIFICATION SUMMARY

DATE: ~08/10/2005

PATENT APPLICATION: US/09/545,998B

TIME: 14:51:49

Input Set : N:\AMC\PTO.AMC.txt

Output Set: N:\CRF4\08102005\I545998B.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

Raw Sequence Listing before editing, for reference only



IFW16

RAW SEQUENCE LISTING DATE: 08/10/2005
PATENT APPLICATION: US/09/545,998B TIME: 09:42:45

Input Set : D:\14094-20005.10 - corrected seq list (original from

client).txt

Output Set: N:\CRF4\08102005\I545998B.raw

SEQUENCE LISTING (1) GENERAL INFORMATION: (i) APPLICANT: Gorman, Daniel M. 6 7 Randall, Troy D. 8 Zlotnik, Albert 10 (ii) TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED 11 REAGENTS (iii) NUMBER OF SEQUENCES: 9 13 15 (iv) CORRESPONDENCE ADDRESS: 16 (A) ADDRESSEE: DNAX Research Institute 17 (B) STREET: 901 California Avenue 18 (C) CITY: Palo Alto Does Not Comply Corrected Diskette Neede 19 (D) STATE: California 20 (E) COUNTRY: USA 21 (F) ZIP: 94304-1104 23 (v) COMPUTER READABLE FORM: 24 (A) MEDIUM TYPE: CD-R 25 (B) COMPUTER: IBM PC compatible 26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS 27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 29 (vi) CURRENT APPLICATION DATA: C--> 30 (A) APPLICATION NUMBER: US/09/545,998B C--> 31 (B) FILING DATE: 10-Apr-2000 32 (C) CLASSIFICATION: 42 (vii) PRIOR APPLICATION DATA: 35 (A) APPLICATION NUMBER: US 08/911,423 36 (B) FILING DATE: 16-AUG-1996 39 (A) APPLICATION NUMBER: US 60/023,419 40 (B) FILING DATE: 16-AUG-1996 43 (A) APPLICATION NUMBER: US 60/027,901 44 (B) FILING DATE: 07-OCT-1996 46 (viii) ATTORNEY/AGENT INFORMATION: (A) NAME: Hill, Laurie L. 47 48 (B) REGISTRATION NUMBER: 51,804 49 (C) REFERENCE/DOCKET NUMBER: 140942000510 51 (ix) TELECOMMUNICATION INFORMATION: 52 (A) TELEPHONE: 858-720-5100

ERRORED SEQUENCES

53

(P.)

590 (2) INFORMATION FOR SEQ ID NO: 9:

(B) TELEFAX: 858-720-5125

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RAW SEQUENCE LISTING
                                                             DATE: 08/10/2005
                     PATENT APPLICATION: US/09/545,998B
                                                              TIME: 09:42:45
                     Input Set : D:\14094-20005.10 - corrected seq list (original from
client).txt
                     Output Set: N:\CRF4\08102005\1545998B.raw
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              (i) SEQUENCE CHARACTERISTICS:
     593
                   (A) LENGTH: 6 amino acids
     594
                   (B) TYPE: amino acid
     595
                   (C) STRANDEDNESS: single
     596
                   (D) TOPOLOGY: linear
     598
             (ii) MOLECULE TYPE: peptide
     602
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
     604
              His His His His His
     605
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VERIFICATION SUMMARY

DATE: 08/10/2005

PATENT APPLICATION: US/09/545,998B

TIME: 09:42:46

Input Set : D:\14094-20005.10 - corrected seq list (original from

client).txt

Output Set: N:\CRF4\08102005\I545998B.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:] L:609 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9

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